



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott
YAMAJI, Noboru

(ii) TITLE OF INVENTION: RECEPTOR PROTEINS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute Inc.- Legal Affairs
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/123,934
(B) FILING DATE: 17-SEP-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: LAZAR, Steven R
(B) REGISTRATION NUMBER: 32,618
(C) REFERENCE/DOCKET NUMBER: 5203

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617 876 1170
(B) TELEFAX: 617 876 5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: CFK1-23a

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 61..1656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGTGGATC CCCCGGGCTG CAGGAATTCT GCGGCCGCCA GGACACGTGC GAATTGGACA	60
ATG ACT CAG CTA TAC ACT TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC	108
Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe	
1 5 10 15	
ATC ATT TCT CAT GTT CAA GGG CAG AAT CTA GAT AGT ATG CTC CAT GGT	156
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly	
20 25 30	
ACT GGT ATG AAA TCA GAC GTG GAC CAG AAG CCG GAA AAT GGA GTG	204
Thr Gly Met Lys Ser Asp Val Asp Gln Lys Lys Pro Glu Asn Gly Val	
35 40 45	
ACG TTA GCA CCA GAG GAC ACC TTA CCT TTC TTA AAA TGC TAT TGC TCA	252
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser	
50 55 60	
GGA CAC TGC CCA GAT GAC GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC	300
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly	
65 70 75 80	
CAT TGC TTT GCC ATT ATA GAA GAA GAT GAT CAG GGA GAA ACC ACG TTA	348
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu	
85 90 95	
ACT TCT GGG TGT ATG AAG TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT	396
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp	
100 105 110	
TCA CCA AAA GCC CAG CTA CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT	444
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn	
115 120 125	
TTG TGC AAC CAA TAT TTG CAG CCT ACA CTG CCC CCT GTC GTT ATA GGC	492
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly	
130 135 140	
CCA TTC TTT GAT GGC AGC GTC CGA TGG CTG GCT GTG CTC ATC TCT ATG	540
Pro Phe Phe Asp Gly Ser Val Arg Trp Leu Ala Val Leu Ile Ser Met	
145 150 155 160	
GCT GTC TGT ATT GTC GCC ATG ATC GTC TTC TCC AGC TGC TTC TGT TAC	588
Ala Val Cys Ile Val Ala Met Ile Val Phe Ser Ser Cys Phe Cys Tyr	
165 170 175	
AAA CAT TAC TGT AAG AGT ATC TCA AGC AGA GGT CGT TAC AAC CGT GAC	636
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp	
180 185 190	
TTG GAA CAG GAT GAA GCA TTT ATT CCA GTA GGA GAA TCA CTG AAA GAC	684
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp	
195 200 205	
CTG ATT GAC CAG TCA CAA AGC TCT GGT AGT GGA TCT GGA TTA CCT TTA	732
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu	
210 215 220	

TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val 225 230 235 240	780
GGT AAG GGC CGG TAT GGA GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu 245 250 255	828
AAA GTG GCT GTC AAA GTA TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe 260 265 270	876
AGA GAA ACA GAA ATC TAC CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile 275 280 285	924
CTT GGT TTT ATA GCT GCA GAC ATT AAA GGC ACC GGT TCC TGG ACT CAG Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln 290 295 300	972
CTG TAT TTG ATT ACT GAT TAC CAT GAG AAT GGG TCT CTC TAT GAC TTC Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe 305 310 315 320	1020
CTG AAA TGT GCC ACC CTG GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr 325 330 335	1068
TCT GCT GCC TGT GGT CTG TGC CAC CTC CAC ACA GAA ATT TAT GGC ACG Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr 340 345 350	1116
CAA GCC AAG CCT GCA ATT GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile 355 360 365	1164
CTT ATT AAG AAA AAT GGT AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala 370 375 380	1212
GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAC ATA CCC TTG AAC ACC Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr 385 390 395 400	1260
AGG GTG GGC ACC AGG CGG TAC ATG GCT CCA GAA GTG CTG GAC GAG AGC Arg Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser 405 410 415	1308
CTG AGT AAA AAC CAT TTC CAG CCC TAC ATC ATG GCT GAC ATC TAC AGC Leu Ser Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser 420 425 430	1356
TTT GGT TTG ATC ATT TGG GAG ATG GCC CGT CGC TGT ATT ACA GGA GGA Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly 435 440 445	1404
ATC GTG GAG GAA TAT CAA TTA CCA TAT TAC AAC ATG GTG CCT AGT GAC Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp 450 455 460	1452

CCA TCT TAT GAA GAC ATG CGT GAG GTC GTG TGT GTG AAA CGC TTG CGG Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg 465 470 475 480	1500
CCA ATC GTC TCT AAC CGC TGG AAC AGT GAT GAA TGT CTT CGA GCC GTT Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val 485 490 495	1548
TTG AAG CTG ATG TCA GAA TGC TGG GCC CAT AAT CCA GCA TCC AGA CTC Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu 500 505 510	1596
ACA GCT TTG AGA ATC AAG AAG ACG CTC GCA AAG ATG GTT GAA TCC CAG Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln 515 520 525	1644
GAT GTA AAG ATT TGACAAACAG TTTTGAGAAA GAATTTAGAC TGCAAGAAAAT Asp Val Lys Ile 530	1696
TCACCCGAGG AAGGGTGGAG TTAGCATGGA CTAGGATGTC GGCTTGGTTT CCAGACTCTC TCCTCTACCA TCTTCACAGG CTGCTAACAG TAAACCTTTC AGGACTCTGC AGAATGC	1756
	1813

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe 1 5 10 15
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly 20 25 30
Thr Gly Met Lys Ser Asp Val Asp Gln Lys Lys Pro Glu Asn Gly Val 35 40 45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser 50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly 65 70 75 80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu 85 90 95
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp 100 105 110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn 115 120 125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly 130 135 140

Pro Phe Phe Asp Gly Ser Val Arg Trp Leu Ala Val Leu Ile Ser Met
 145 150 155 160
 Ala Val Cys Ile Val Ala Met Ile Val Phe Ser Ser Cys Phe Cys Tyr
 165 170 175
 Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
 180 185 190
 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
 195 200 205
 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Leu Pro Leu
 210 215 220
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
 225 230 235 240
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
 245 250 255
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
 260 265 270
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
 275 280 285
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
 290 295 300
 Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
 305 310 315 320
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
 325 330 335
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
 340 345 350
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
 355 360 365
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Ser Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480

Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495

Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
500 505 510

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525

Asp Val Lys Ile
530

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) IMMEDIATE SOURCE:

(B) CLONE: CFK1-43a

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 247..1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTT CAA TGT CGC GAC ACG CCC ATC CCT CAT CAG AGA AGG TCA ATT GAA Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu 80 85 90	528
TGC TGC ACA GAA AGG AAC GAA TGT AAT AAA GAT CTC CAC CCC ACG CTG Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu 95 100 105 110	576
CCT CCC CTG AAG GAC AGA GAT TTT GTT GAT GGA CCC ATA CAC CAC AAA Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys 115 120 125	624
GCC TTA CTC ATA TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile 130 135 140	672
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC AGA CCT CGG Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg 145 150 155	720
TAC AGC ATT GGG CTG GAG CAG GAT GAA ACG TAC ATT CCT CCT GGA GAA Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu 160 165 170	768
TCC CTG AGA GAC TTG ATT GAG CAA TCG CAG AGC TCG GGA AGT GGC TCA Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser 175 180 185 190	816
GGA CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met 195 200 205	864
GTG AAG CAA ATT GGA AAA GGT CGC TAT GGC GAA GTG TGG ATG GGA AAG Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys 210 215 220	912
TGG CGT GGA GAA AAG GTA GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu 225 230 235	960
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG AGG Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg 240 245 250	1008
CAC GAG AAC ATT CTG GGG TTC ATT GCA GCA GAT ATC AAA GGG ACT GGG His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly 255 260 265 270	1056
TCT TGG ACT CAG TTA TAC CTC ATC ACA GAC TAT CAT GAA AAC GGG TCT Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser 275 280 285	1104
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAT GCC AAG TCC ATG CTG Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu 290 295 300	1152
AAG CTA GCC TAC TCG TCT GTC AGC GGC CTG TGC CAT CTA CAC ACG GAA Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu 305 310 315	1200

ATC TTC AGC ACT CAA GGC AAG CCA GCC ATT GCC CAT CGG GAC TTG AAA Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys 320 325 330	1248
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp 335 340 345 350	1296
CTG GGC CTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATT Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile 355 360 365	1344
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val 370 375 380	1392
CTG GAC GAG AGC TTG AAT AGA ACT CAT TTC CAG TCC TAC ATC ATG GCT Leu Asp Glu Ser Leu Asn Arg Thr His Phe Gln Ser Tyr Ile Met Ala 385 390 395	1440
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys 400 405 410	1488
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCA TAT CAC GAC CTG Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu 415 420 425 430	1536
GTG CCC AGT GAC CCC TCT TAT GAG GAC ATG AGA GAA ATT GTG TGT ATG Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met 435 440 445	1584
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAC GAG TGC Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys 450 455 460	1632
CTC AGG CAA ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAT AAT CCT Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro 465 470 475	1680
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACA CTT GCC AAA ATG Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met 480 485 490	1728
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGG TACTTGTGGA CAGAGCAAGG Ser Glu Ser Gln Asp Ile Lys Leu 495 500	1782
AATTACACAG AAGCATCCTT AGCCCAAGCC TTGAACGTTG ATCTACTGCC CAGTGAGTTC AGACTTTCTT CTAAGAGAGC AAGCTGGACA GACACAGAGG AACCCAGAAA CACGGCTTCA CCATGGCTTT CTGAGGAGGG GAAACCATTG GGGTAACCTG TTCAAGATAT GATGCATGTT GCTTTCTAAG AAAGCCCTGT ATTTTGGGAT TACCATTTTT TTTAAAGAAG AAAGATACTT TAATTTTAC CAAAATAAAA CAAATATTAT AGAAAAAAAG CGGCCGCAGA ATTC	1842 1902 1962 2022 2076

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
 1 5 10 15

Asp Gly Glu Ser Thr Ala Pro Thr Ala Arg Pro Lys Val Leu Arg Cys
 20 25 30

Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
 35 40 45

Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Thr
 50 55 60

Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
 65 70 75 80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
 85 90 95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110

Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
 115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
 145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Leu
 180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325 330 335
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340 345 350
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380
 Glu Ser Leu Asn Arg Thr His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
 405 410 415
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
 420 425 430
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
 435 440 445
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
 450 455 460
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro Ala Ser
 465 470 475 480
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
 485 490 495
 Ser Gln Asp Ile Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CFKL-10a

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 474..2000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTGCG	GCCGCGAGGC	TGCATTAAGT	GGGATATGCC	ACCCGTGATT	CTGACAGCCG	60
TGACTGCGTG	GAGCCTGCTC	CGGAACCTCTC	CACAGAGGAG	CAAAGGAGCT	GCCCTCTGTG	120
TCTCCCCGCC	CTTCAGCGAG	AGTCTGGAAA	GAGAACCGAG	GTGCTACTGC	AGTGGATGAG	180
TAGAGAAGAG	TCTGCATCCA	GTGCTGGTGA	GCTTGTCTGG	CTATAGGGAG	CCTGCTGGGG	240
GAAACTTACA	GCTTCAGAAG	ACTCCTGGAG	AGCCTCTCCC	TCCACACTCT	CCCTTGAGC	300
AGTCAGTGCC	TCTCTGCTGG	AGAACCTGTG	CTGGGTGTGC	CCCAGAGCTG	GCTTTGACTG	360
TAGCCTGTCA	GGCTCTCCCT	GGACCTCACG	GAACAGCATT	GCCAGCCACA	CGGCTTCCAA	420
CAAATCACCT	CTTTTCATGC	TGTTTGGCAC	AGATCGAAC	TACAGGTTAT	ACA ATG	476
				Met		
				1		
GTC GAT GGA GCA ATG ATC CTT TCT GTG CTA ATG ATG ATG GCT CTC CCT						524
Val Asp Gly Ala Met Ile Leu Ser Val Leu Met Met Met Ala Leu Pro						
5	10			15		
TCC CCG AGT ATG GAA GAT GAG GAG CCC AAG GTC AAC CCG AAG CTT TAC						572
Ser Pro Ser Met Glu Asp Glu Glu Pro Lys Val Asn Pro Lys Leu Tyr						
20	25			30		
ATG TGT GTG TGT GAG GGC CTC TCC TGC GGG AAC GAG GAC CAC TGT GAG						620
Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu						
35	40			45		
GGC CAG CAG TGT TTT TCC TCC CTG AGC GTC AAT GAT GGC TTC CGC GTC						668
Gly Gln Gln Cys Phe Ser Ser Leu Ser Val Asn Asp Gly Phe Arg Val						
50	55			60		65
TAC CAG AAG GGC TGC TTT CAG GTC TAT GAG CAG GGG AAG ATG ACG TGT						716
Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys						
70	75			80		
AAG ACC CCG CCG TCG CCT GGC CAG GCT GTG GAG TGC TGC CAA GGG GAC						764
Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp						
85	90			95		
TGG TGC AAC AGG AAC GTC ACG GCC CGG CTG CCC ACT AAA GGG AAA TCC						812
Trp Cys Asn Arg Asn Val Thr Ala Arg Leu Pro Thr Lys Gly Lys Ser						
100	105			110		
TTC CCT GGA TCG CAG AAC TTC CAC CTG GAA GTT GGC CTT ATC ATC CTC						860
Phe Pro Gly Ser Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu						
115	120			125		
TCC GTG GTG TTT GCG GTA TGC CTT TTC GCT TGC ATC CTT GGC GTT GCT						908
Ser Val Val Phe Ala Val Cys Leu Phe Ala Cys Ile Leu Gly Val Ala						
130	135			140		145
CTC AGG AAG TTT AAA AGG CGC AAT CAA GAG CGC CTG AAC CCC AGA GAC						956
Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp						
150	155			160		

GTG GAG TAC GGT ACT ATC GAA GGG CTC ATC ACC ACC AAC GTC GGA GAT Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp 165 170 175	1004
AGC ACT CTA GCG GAA TTA CTA GAT CAC TCA TGT ACA TCA GGA AGT GGC Ser Thr Leu Ala Glu Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly 180 185 190	1052
TCC GGT CTT CCT TTT CTG GTA CAG AGA ACT GTG GCT CGA CAG ATA ACC Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr 195 200 205	1100
CTG TTG GAG TGT GTC GGG AAG GGC CGG TAT GGA GAA GTG TGG AGG GGC Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly 210 215 220 225	1148
AGC TGG CAA GGC GAA AAT GTT GCT GTG AAG ATC TTC TCC TCC CGT GAT Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp 230 235 240	1196
GAG AAG TCG TGG TTC AGG GAG ACA GAA TTG TAC AAC ACG GTG ATG CTG Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu 245 250 255	1244
AGG CAT GAG AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACC TCT AGA Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg 260 265 270	1292
CAC TCC AGT ACC CAG CTG TGG CTC ATT ACA CAT TAC CAC GAA ATG GGA His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly 275 280 285	1340
TCG TTG TAT GAC TAC CTT CAG CTC ACC ACT CTG GAC ACC GTT AGC TGC Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys 290 295 300 305	1388
CTT CGG ATC GTG TTG TCC ATA GCC AGC GGC CTT GCA CAC TTG CAC ATA Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile 310 315 320	1436
GAG ATA TTT GGG ACC CAG GGG AAG TCT GCC ATC GCC CAC CGA GAT CTA Glu Ile Phe Gly Thr Gln Gly Lys Ser Ala Ile Ala His Arg Asp Leu 325 330 335	1484
AAG AGC AAA AAC ATC CTC GTG AAG AAG AAC GGA CAG TGC TGC ATA GCA Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala 340 345 350	1532
GAT TTG GGC CTG GCA GTC ATG CAT TCC CAG AGC ACG AAT CAG CTT GAT Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp 355 360 365	1580
GTG GGA AAC AAC CCC CGT GTG GGG ACC AAG CGC TAC ATG GCC CCT GAA Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu 370 375 380 385	1628
GTG CTT GAT GAA ACC ATC CAA GTG GAT TGC TTT GAT TCT TAT AAG AGG Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg 390 395 400	1676

GTC GAT ATT TGG GCC TTT GGC CTC GTT CTG TGG GAA GTG GCC AGG AGG Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg 405 410 415	1724
ATG GTG AGC AAT GGT ATA GTG GAA GAT TAC AAG CCA CCA TTC TAT GAT Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp 420 425 430	1772
GTT GTT CCC AAT GAC CCA AGT TTT GAA GAT ATG AGG AAA GTT GTC TGT Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys 435 440 445	1820
GTG GAT CAA CAG AGG CCA AAC ATA CCT AAC AGA TGG TTC TCA GAC CCG Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro 450 455 460 465	1868
ACA TTA ACT TCT CTG GCG AAG CTG ATG AAA GAA TGC TGG TAC CAG AAC Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn 470 475 480	1916
CCA TCC GCC AGA CTC ACA GCT CTA CGT ATC AAA AAG ACT TTG ACC AAA Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys 485 490 495	1964
ATT GAT AAC TCC CTA GAC AAA TTA AAA ACT GAC TGT TGACATTGTC Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys 500 505	2010
ACCGGTGTCA AGAAGGAGAG TCAATGCTGT CATTGTCCAG CTGGGACCTA ATGCTGGCCT GACTGGTTGT CAGAACAGAA TCCATCTGTC CCCCTCTCCC CCCAACTCCC GAAGTGGCTG CTTGACAAA AGCAGATGTC TCTTCCCAGC CATGTTCCGG GGGAGACACC AAAACCACCC TAACCTCGCT CAGAAACTGT GACTCGAGCA CTTGATGAAC TGTTCACACC GCAGAACTCA ACGGTGGGCA GGTATGTTTG CAAGGGGGAG GGAAGTGGAG GAGCACAGAG AGATCCTGCA GGAGATCTGG GCATTAGGAC AGTGGCTCTT TGCCTATCTT CCACGGGTCT CCTAGACTCG CCCCACGGGA AACTCAAGGA GGCGGTGAAT TCGTAATCAG CAATATTGGC TGCGCCTACT CTTCTCTGTT GCACTAGGAA TTCTCTGCAT TCCTTACTTG CACTGTGTC CTTAATCTTA AAGACCCGAC TTGCCAAAAC ATTGGCTGCC TACTTCACTG GCCTGTCTCT GGACAATAGG AATTCAATCT GGCGAAACAA AAATGTAATG TTGGACTTTG CTGCATTTA CACACGTGCC GATGTTACA ACGATGCAA CATTAGGAAT TGTTAGACA CAACTTGCA AATTATTTAT TACTGGTGCA CTTAGCAGTT TTTGTTTTT TTTGTTTTT TGTTTTTTT TTGTTTGTT TTGTTTTAT ATATAAAACT GCCTCGTGCG TATGTTAAAG CTTATTTTA TGTGGTCTTA TGATTTATT ACCGAAATGT TTTAACACC CGATTCTGAA ATGGATGTT TCTTTTATTA TCAGTTAAAT TCACATTTA AATGCTTCAC TTTTTTTTA TGTGTGAGA CTGTAACCTT CTTTTCAGTT AGTATACAGA ACGTATTTAG CCATTACCCA TGCAACACCA CCCAATATAT TACTGATTAA GAAGCAAAGA TTTCAGTAGA ATTTTAGTCC CAAACGCTGT GGGGGGAAA	2070 2130 2190 2250 2310 2370 2430 2490 2550 2610 2670 2730 2790 2850 2910 2970 3030

TGCATCTTCT TCGGAACATAT CCATTACATG CATTAAACT CTGCCAGAAA AAAAAATAAC	3090
TATTTTGTTC TAATCTACTT TTTGTATTT GTAGTTATTT GTATAAATTA AATAAACTGT	3150
TTTCAAGTCA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAAT	3210
AAAAAAA AAAGCGGCCG CAGAATTC	3238

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Asp Gly Ala Met Ile Leu Ser Val Leu Met Met Met Ala Leu	
1 5 10 15	
Pro Ser Pro Ser Met Glu Asp Glu Glu Pro Lys Val Asn Pro Lys Leu	
20 25 30	
Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys	
35 40 45	
Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Val Asn Asp Gly Phe Arg	
50 55 60	
Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr	
65 70 75 80	
Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly	
85 90 95	
Asp Trp Cys Asn Arg Asn Val Thr Ala Arg Leu Pro Thr Lys Gly Lys	
100 105 110	
Ser Phe Pro Gly Ser Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile	
115 120 125	
Leu Ser Val Val Phe Ala Val Cys Leu Phe Ala Cys Ile Leu Gly Val	
130 135 140	
Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg	
145 150 155 160	
Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly	
165 170 175	
Asp Ser Thr Leu Ala Glu Leu Leu Asp His Ser Cys Thr Ser Gly Ser	
180 185 190	
Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile	
195 200 205	
Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg	
210 215 220	

Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
 225 230 235 240
 Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
 245 250 255
 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
 260 265 270
 Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
 275 280 285
 Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
 290 295 300
 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 305 310 315 320
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Ser Ala Ile Ala His Arg Asp
 325 330 335
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 340 345 350
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 355 360 365
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 370 375 380

 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 385 390 395 400
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 405 410 415
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 420 425 430
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 435 440 445
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: W-101

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 80..1594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATCTGCGG CCGCGAGGGA GAGAGGCGCC GGGGGCGCGC GCGCGCGCTG GGCGCTGCTG	60
GGCTGCGGGG GCGGTTACT ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC	112
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe	
1 5 10	
CCC CTT GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG	160
Pro Leu Val Val Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg	
15 20 25	
GGG ATC CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC	208
Gly Ile Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn	
30 35 40	
TAC ACC TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG	256
Tyr Thr Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu	
45 50 55	
GAT GGC GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG	304
Asp Gly Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu	
60 65 70 75	
GTT CCT GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC	352
Val Pro Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg	
80 85 90	
AAC ACA CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG	400
Asn Thr His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg	
95 100 105	
GTC CCC AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC	448
Val Pro Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly	
110 115 120	
CCT GTG GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC	496
Pro Val Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe	
125 130 135	
CTT ATC ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC	544
Leu Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val	
140 145 150 155	
TAC CAT AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG	592
Tyr His Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met	
160 165 170	

TGT CTC TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC	640
Cys Leu Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser	
175 180 185	
ACG TCA GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG	688
Thr Ser Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val	
190 195 200	
GCC CGA ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG	736
Ala Arg Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly	
205 210 215	
GAA GTA TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC	784
Glu Val Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile	
220 225 230 235	
TTC TCT TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC	832
Phe Ser Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr	
240 245 250	
CAG ACC GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT	880
Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala	
255 260 265	
GAC AAT AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC	928
Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp	
270 275 280	
TAT CAC GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACC GTG	976
Tyr His Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val	
285 290 295	
ACC ATT GAG GGC ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG	1024
Thr Ile Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu	
300 305 310 315	
GCA CAC CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT	1072
Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile	
320 325 330	
GCT CAT CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC	1120
Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly	
335 340 345	
ATG TGT GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC	1168
Met Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val	
350 355 360	
ACT GAC ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA	1216
Thr Asp Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg	
365 370 375	
TAC ATG GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT	1264
Tyr Met Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe	
380 385 390 395	
GAC TCC TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG	1312
Asp Ser Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp	
400 405 410	

GAG ATT GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA Glu Ile Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln 415 420 425	1360
CTG CCG TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG Leu Pro Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met 430 435 440	1408
CGA AAG GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp 445 450 455	1456
TGG CAG AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG Trp Gln Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu 460 465 470 475	1504
TGC TGG TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys 480 485 490	1552
AAG ACT CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT Lys Thr Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile 495 500 505	1594
TAAGCTGTTA AGATGCCTAC ACAAAAGAACCC TGGGCAGTGA GGATGACTGC AGG	
1647	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu 1 5 10 15
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu 20 25 30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr 35 40 45
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His 50 55 60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys 65 70 75 80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys 85 90 95
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His 100 105 110
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val 115 120 125

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
 130 135 140
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
 145 150 155 160
 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
 165 170 175
 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
 180 185 190
 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
 195 200 205
 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
 210 215 220
 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
 225 230 235 240
 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
 245 250 255
 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
 260 265 270
 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
 275 280 285
 Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
 290 295 300
 Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
 305 310 315 320
 Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
 325 330 335
 Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
 340 345 350
 Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
 355 360 365
 Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
 370 375 380
 Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
 385 390 395 400
 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
 405 410 415
 Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp
 420 425 430
 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
 435 440 445
 Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu
 450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
 465 470 475 480
 Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
 485 490 495
 Leu Ser Val Gln Glu Asp Val Lys Ile
 500 505

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: W-120

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 83..1591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGCGG CCGCGGGCGA GGCTTCCTGA GGAGAAGCTG CGGCCGGGGC CGGGCCGGGC	60
CACAAACAGT GGCGGCGGGA CC ATG GAG GCG GCG GCC GCT GCT CCA CGT CGT	112
Met Glu Ala Ala Ala Ala Pro Arg Arg	
1 5 10	
CCG CAG CTC CTC ATC GTG TTG GTG GCG GCG GCG ACG CTG CTC CCG GGG	160
Pro Gln Leu Leu Ile Val Leu Val Ala Ala Ala Thr Leu Leu Pro Gly	
15 20 25	
GCG AAG GCA TTA CAG TGT TTC TGC CAC CTC TGT ACA AAG GAT AAT TTT	208
Ala Lys Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe	
30 35 40	
ACC TGT GAG ACA GAT GGT CTT TGC TTT GTC TCA GTC ACT GAG ACC ACA	256
Thr Cys Glu Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr	
45 50 55	
GAC AAA GTT ATA CAC AAT AGT ATG TGT ATA GCT GAA ATT GAC CTA ATT	304
Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile	
60 65 70	
CCT CGA GAC AGG CCA TTT GTC TGT GCA CCA TCT TCA AAA ACA GGG GCA	352
Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ala	
75 80 85 90	
GTT ACT ACA ACA TAT TGC TGC AAT CAG GAC CAC TGC AAT AAA ATA GAA	400
Val Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu	
95 100 105	
CTC CCA ACT ACA GGA CCT TTT TCA GAA AAG CAG TCA GCT GGC CTT GGT	448
Leu Pro Thr Thr Gly Pro Phe Ser Glu Lys Gln Ser Ala Gly Leu Gly	
110 115 120	

CCT GTG GAG CTG GCA GCT GTC ATT GCT GGT CCA GTC TGC TTC GTC TGC Pro Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys 125 130 135	496
ATT GCA CTT ATG CTG ATG GTC TAT ATC TGC CAT AAC CGC ACT GTC ATT Ile Ala Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile 140 145 150	544
CAC CAC CGT GTG CCA AAT GAA GAG GAT CCA TCA CTA GAT CGC CCT TTC His His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe 155 160 165 170	592
ATT TCA GAG GGC ACC ACC TTA AAA GAT TTA ATT TAT GAT ATG ACA ACA Ile Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr 175 180 185	640
TCA GGG TCT GGA TCA GGT TTA CCA CTG CTT GTT CAA AGA ACA ATT GCC Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala 190 195 200	688
AGG ACC ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGG TTT GGA GAA Arg Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu 205 210 215	736
GTT TGG CGA GGC AAA TGG CGG GGA GAA GAA GTT GCT GTG AAG ATA TTC Val Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe 220 225 230	784
TCT TCT AGA GAA GAG CGT TCA TGG TTC CGA GAG GCA GAG ATT TAT CAG Ser Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln 235 240 245 250	832
ACT GTA ATG TTA CGC CAT GAA AAT ATC CTG GGA TTT ATA GCA GCA GAC Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp 255 260 265	880
AAC AAA GAC AAT GGG ACA TGG ACG CAG CTG TGG TTG GTG TCA GAT TAT Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr 270 275 280	928
CAT GAG CAT GGA TCC CTT TTC GAT TAC TTG AAT AGA TAC ACT GTT ACT His Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr 285 290 295	976
GTG GAA GGA ATG ATC AAG CTT GCT CTG TCC ACA GCA AGT GGT CTT GCC Val Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala 300 305 310	1024
CAT CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAA CCA GCT ATT GCC His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala 315 320 325 330	1072
CAT AGA GAT TTG AAA TCA AAG AAT ATC TTG GTG AAG AAA AAT GGA ACC His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr 335 340 345	1120
TGT TGT ATT GCA GAC TTG GGA CTT GCT GTG AGA CAT GAT TCT GCC ACA Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr 350 355 360	1168

GAT ACA ATT GAT ATT GCT CCA AAC CAC AGA GTA GGC ACT AAA AGG TAC Asp Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr 365 370 375	1216
ATG GCC CCT GAA GTT CTA GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA Met Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu 380 385 390	1264
TCC TTC AAA CGC GCT GAC ATC TAT GCA ATG GGC TTA GTG TTC TGG GAA Ser Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu 395 400 405 410	1312
ATT GCT CGA CGC TGT TCT ATT GGT GGA ATC CAT GAA GAC TAT CAG TTG Ile Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu 415 420 425	1360
CCT TAT TAT GAT CTT GTA CCT TCT GAT CCA TCG GTT GAA GAA ATG AGA Pro Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg 430 435 440	1408
AAA GTA GTT TGC GAA CAG AAG TTA AGG CCA AAT ATT CCA AAC AGA TGG Lys Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp 445 450 455	1456
CAG AGC TGT GAG GCC TTG AGA GTG ATG GCT AAA ATT ATG AGA GAA TGC Gln Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys 460 465 470	1504
TGG TAT GCC AAT GGA GCA GCA AGG CTG ACA GCT TTG CGA ATT AAA AAA Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys 475 480 485 490	1552
ACA TTG TCA CAA CTC AGC CAA CAG GAA GGC ATC AAA ATG TAACTGAAAC Thr Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met 495 500	1601
ACCGTGGAA CTCTGCTCTC TTCAATCTG CTCCTGGTG TTTAGGAGGC TGGTTGTTCT	1661
ACCTCACTGA GAGAACAGAG GGCTCTGCTT CCTCTTGCAG CAGTGGAAATA TGGTCAACTG	1721
AAAGCTTCCC AGGGTTCTC TGGGCCAGA GGCAGCCGTG GGGTCCTTCT GTGCACTATG	1781
GATAACTTCT TCC	1794

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Ala Ala Ala Ala Pro Arg Arg Pro Gln Leu Leu Ile Val 1 5 10 15
Leu Val Ala Ala Ala Thr Leu Leu Pro Gly Ala Lys Ala Leu Gln Cys 20 25 30

Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Glu Thr Asp Gly
 35 40 45
 Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val Ile His Asn
 50 55 60
 Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp Arg Pro Phe
 65 70 75 80
 Val Cys Ala Pro Ser Ser Lys Thr Gly Ala Val Thr Thr Tyr Cys
 85 90 95
 Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr Thr Gly Pro
 100 105 110
 Phe Ser Glu Lys Gln Ser Ala Gly Leu Gly Pro Val Glu Leu Ala Ala
 115 120 125
 Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ala Leu Met Leu Met
 130 135 140
 Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
 145 150 155 160
 Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
 165 170 175
 Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
 180 185 190
 Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
 195 200 205
 Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
 210 215 220
 Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
 225 230 235 240
 Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
 245 250 255
 Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
 260 265 270
 Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu
 275 280 285
 Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
 290 295 300
 Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
 305 310 315 320
 Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
 325 330 335
 Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
 340 345 350
 Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
 355 360 365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370 375 380
 Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
 385 390 395 400
 Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
 405 410 415
 Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
 420 425 430
 Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
 435 440 445
 Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
 450 455 460
 Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
 485 490 495
 Gln Gln Glu Gly Ile Lys Met
 500

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- vii) IMMEDIATE SOURCE:
 - (B) CLONE: KDA-B5
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 25..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATCCGAAT	ACGTGGCGGT	TAAA	ATA	TTC	TCC	TCC	AGG	GAT	GAG	AGA	TCT	51				
			Ile	Phe	Ser	Ser	Arg	Asp	Glu	Arg	Ser					
			1				5									
TGG	TTC	CGT	GAG	GCG	GAA	ATT	TAT	CAG	ACG	GTG	ATG	CTG	AGA	CAC	GAG	99
Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His	Glu	
10			15					20					25			
AAC	ATC	CTC	GGT	TTC	ATC	GCA	GCT	GAC	AAC	AAA	GAT	AAT	GGA	ACT	TGG	147
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr	Trp	
			30					35					40			
ACA	CAA	CTC	TGG	CTT	GTG	TCA	GAG	TAT	CAC	GAG	CAG	GGC	TCC	TTG	TAT	195
Thr	Gln	Leu	Trp	Leu	Val	Ser	Glu	Tyr	His	Glu	Gln	Gly	Ser	Leu	Tyr	
			45				50						55			

GAC TAT TTG AAC AGA AAC ATA GTG ACT GTG GCT GGA ATG GTC AAG CTG Asp Tyr Leu Asn Arg Asn Ile Val Thr Val Ala Gly Met Val Lys Leu 60 65 70	243
GCG CTT TCC ATA GCG AGT GGT CTG GCT CAC CTG CAC ATG GAG ATC GTG Ala Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Met Glu Ile Val 75 80 85	291
GGT ACT CAA GGT AAG CTT GCT ATT GCT CACGGTGATA TCAAAAGTCT Gly Thr Gln Gly Lys Leu Ala Ile Ala 90 95	338
AGA	341

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Phe Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile 1 5 10 15
Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala 20 25 30
Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser 35 40 45
Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile 50 55 60
Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser Gly 65 70 75 80
Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Leu Ala 85 90 95

Ile Ala

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PRIMER A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGGATCCGA RTAYGTNGCN GTNAAR

26

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PRIMER B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACTGTAGAR CTYTTDATRT CYCRTL

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PRIMER C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GACTCTAGAR CTYTTDATRT CNCGR

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PRIMER D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACTCTAGNG AYTTDATRTC YCRT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: PRIMER E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GA~~CT~~CTAGAN GAYTTDATRT CNCGRTG

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: PEPTIDE SEQUENCE OF KDA-B5 USED TO DESIGN
PRIMER A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Glu Tyr Val Ala Val Lys
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: PEPTIDE SEQUENCE OF KDA-B5 USED TO DESIGN
PRIMERS B THRU E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Arg Asp Ile Lys Ser
1 5